



#4

SEQUENCE LISTING

<110> Boetsch, Paul W.
Avery, Angela M.
Kaur, Balveen

<120> Broad Specificity DNA Damage Endonuclease

<130> 25-98A

<140> US/09/724,296

<141> 2000-11-28

<150> US/09/327,984

<151> 1999-06-08

<150> US/60/088,521

<151> 1998-06-08

<150> US/60/134,752

<151> 1999-05-18

<160> 71

<170> PatentIn Ver. 2.0

<210> 1

<211> 2492

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Coding
sequence for fusion protein of GST signal peptide
and the UVDE protein of Schizosaccharomyces pombe

<400> 1

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tattgatggt gatgttaaat taacacagtc tatggccatc atacgttata tagctgacaa 240
gcacaacatg ttggttgggt gtccaaaaga gcgtgcagag atttcaatgc ttgaaggagc 300
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caaagttgat tttcttagca agctacctga aatgctgaaa atgttcgaag atcgtttatg 420
tcataaaaca tatttaaagt ttgacctgt aaccatcct gacttcatgt tgtatgacgc 480
tcttgatgtt gttttataca tggacccaat gtgcctggat gcgttcccaa aattagtttg 540
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ctctaaacgc attgttttca ccatattaaa acaaaaggca tttaaaggta atcatccttg 780
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tgaaggaagt ttagatttaa tgccattaat cccaactatt cgagaaacct ggacaagaaa 2160
gggaattaca cagaagcaac attactcaga atcggtgat ccaacggcga tttctgggat 2220
gaaacgacgt gctcactctg atagggtgtt tgactttcca ccgtgtgatc ctacaatgga 2280
tctaatagata gaagctaagg aaaaggaaca ggctgtatgt gaattgtgta gacgttatga 2340
gttacaaaat ccaccatgtc ctcttgaaat tatggggcct gaatacgatc aaactcgaga 2400
tgatatttat ccgcccgag ctgaaaagcg tttaactgca agaaaaaggc gtagtagaaa 2460
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<210> 2

<211> 828

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fusion protein
of GST leader peptide and Schizosaccharomyces
pombe UVDE

<400> 2

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Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
      20             25             30

```

```

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe
  35             40             45

```

```

Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp
  50             55             60

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Val	Lys	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	
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His	Asn	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	
				85					90					95		
Leu	Glu	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	
			100					105					110			
Tyr	Ser	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	
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Pro	Glu	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	
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Leu	Asn	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	
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Leu	Asp	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	
				165					170					175		
Lys	Leu	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	
			180					185					190			
Lys	Tyr	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	
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Gln	Ala	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	His	Leu	
		210				215					220					
Val	Pro	Arg	Gly	Ser	Met	Leu	Arg	Leu	Leu	Lys	Arg	Asn	Ile	Gln	Ile	
225					230					235					240	
Ser	Lys	Arg	Ile	Val	Phe	Thr	Ile	Leu	Lys	Gln	Lys	Ala	Phe	Lys	Gly	
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His	Cys	Leu	Pro	Asp	Thr	Leu	Lys	Ser	Leu	Leu	Pro	Met	Ser	Ser	Lys	
		275					280					285				
Thr	Thr	Leu	Ser	Met	Leu	Pro	Gln	Val	Asn	Ile	Gly	Ala	Asn	Ser	Phe	
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Ser	Ala	Glu	Thr	Pro	Val	Asp	Leu	Lys	Lys	Glu	Asn	Glu	Thr	Glu	Leu	
305					310					315					320	
Ala	Asn	Ile	Ser	Gly	Pro	His	Lys	Lys	Ser	Thr	Ser	Thr	Ser	Thr	Arg	
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Lys Arg Ala Arg Ser Ser Lys Lys Lys Ala Thr Asp Ser Val Ser Asp
 340 345 350
 Lys Ile Asp Glu Ser Val Ala Ser Tyr Asp Ser Ser Thr His Leu Arg
 355 360 365
 Arg Ser Ser Arg Ser Lys Lys Pro Val Asn Tyr Asn Ser Ser Ser Glu
 370 375 380
 Ser Glu Ser Glu Glu Gln Ile Ser Lys Ala Thr Lys Lys Val Lys Gln
 385 390 395 400
 Lys Glu Glu Glu Glu Tyr Val Glu Glu Val Asp Glu Lys Ser Leu Lys
 405 410 415
 Asn Glu Ser Ser Ser Asp Glu Phe Glu Pro Val Val Pro Glu Gln Leu
 420 425 430
 Glu Thr Pro Ile Ser Lys Arg Arg Arg Ser Arg Ser Ser Ala Lys Asn
 435 440 445
 Leu Glu Lys Glu Ser Thr Met Asn Leu Asp Asp His Ala Pro Arg Glu
 450 455 460
 Met Phe Asp Cys Leu Asp Lys Pro Ile Pro Trp Arg Gly Arg Leu Gly
 465 470 475 480
 Tyr Ala Cys Leu Asn Thr Ile Leu Arg Ser Met Lys Glu Arg Val Phe
 485 490 495
 Cys Ser Arg Thr Cys Arg Ile Thr Thr Ile Gln Arg Asp Gly Leu Glu
 500 505 510
 Ser Val Lys Gln Leu Gly Thr Gln Asn Val Leu Asp Leu Ile Lys Leu
 515 520 525
 Val Glu Trp Asn His Asn Phe Gly Ile His Phe Met Arg Val Ser Ser
 530 535 540
 Asp Leu Phe Pro Phe Ala Ser His Ala Lys Tyr Gly Tyr Thr Leu Glu
 545 550 555 560
 Phe Ala Gln Ser His Leu Glu Glu Val Gly Lys Leu Ala Asn Lys Tyr
 565 570 575
 Asn His Arg Leu Thr Met His Pro Gly Gln Tyr Thr Gln Ile Ala Ser
 580 585 590
 Pro Arg Glu Val Val Val Asp Ser Ala Ile Arg Asp Leu Ala Tyr His
 595 600 605

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Asp Glu Ile Leu Ser Arg Met Lys Leu Asn Glu Gln Leu Asn Lys Asp
610 615 620

Ala Val Leu Ile Ile His Leu Gly Gly Thr Phe Glu Gly Lys Lys Glu
625 630 635 640

Thr Leu Asp Arg Phe Arg Lys Asn Tyr Gln Arg Leu Ser Asp Ser Val
645 650 655

Lys Ala Arg Leu Val Leu Glu Asn Asp Asp Val Ser Trp Ser Val Gln
660 665 670

Asp Leu Leu Pro Leu Cys Gln Glu Leu Asn Ile Pro Leu Val Leu Asp
675 680 685

Trp His His His Asn Ile Val Pro Gly Thr Leu Arg Glu Gly Ser Leu
690 695 700

Asp Leu Met Pro Leu Ile Pro Thr Ile Arg Glu Thr Trp Thr Arg Lys
705 710 715 720

Gly Ile Thr Gln Lys Gln His Tyr Ser Glu Ser Ala Asp Pro Thr Ala
725 730 735

Ile Ser Gly Met Lys Arg Arg Ala His Ser Asp Arg Val Phe Asp Phe
740 745 750

Pro Pro Cys Asp Pro Thr Met Asp Leu Met Ile Glu Ala Lys Glu Lys
755 760 765

Glu Gln Ala Val Phe Glu Leu Cys Arg Arg Tyr Glu Leu Gln Asn Pro
770 775 780

Pro Cys Pro Leu Glu Ile Met Gly Pro Glu Tyr Asp Gln Thr Arg Asp
785 790 795 800

Gly Tyr Tyr Pro Pro Gly Ala Glu Lys Arg Leu Thr Ala Arg Lys Arg
805 810 815

Arg Ser Arg Lys Glu Glu Val Glu Glu Asp Glu Lys
820 825

<210> 3
<211> 1161
<212> DNA
<213> Schizosaccharomyces pombe

<220>
<221> misc_feature
<222> (1)..(1161)

<223> DNA sequence encoding UVDE protein, truncated at amino acid residue 228.

<400> 3

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tcacgcacct gccgaattac aaccattcaa cgtgatgggc tcgaaagtgt caagcagcta 180
ggtacgcaaa atgtttttaga tttaatcaaa ttggttgagt ggaatcacia ctttggcatt 240
cacttcatga gagtgagttc tgatttattt cctttcgcaa gccatgcaaa gtatggatat 300
acccttgaat ttgcacaatc tcatctcgag gaggtgggca agctggcaaa taaatataat 360
catcgattga ctatgcatcc tggtcagtac acccagatag cctctccacg agaagtcgta 420
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<210> 4

<211> 371

<212> PRT

<213> Schizosaccharomyces pombe

<220>

<221> VARIANT

<222> (1)..(371)

<223> Truncated version of the UVDE protein.

<400> 4

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```

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Pro Trp Arg Gly Arg Leu Gly Tyr Ala Cys Leu Asn Thr Ile Leu Arg
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Ser Met Lys Glu Arg Val Phe Cys Ser Arg Thr Cys Arg Ile Thr Thr
      35              40              45

```

```

Ile Gln Arg Asp Gly Leu Glu Ser Val Lys Gln Leu Gly Thr Gln Asn
      50              55              60

```

```

Val Leu Asp Leu Ile Lys Leu Val Glu Trp Asn His Asn Phe Gly Ile
      65              70              75              80

```

His Phe Met Arg Val Ser Ser Asp Leu Phe Pro Phe Ala Ser His Ala
85 90 95

Lys Tyr Gly Tyr Thr Leu Glu Phe Ala Gln Ser His Leu Glu Glu Val
100 105 110

Gly Lys Leu Ala Asn Lys Tyr Asn His Arg Leu Thr Met His Pro Gly
115 120 125

Gln Tyr Thr Gln Ile Ala Ser Pro Arg Glu Val Val Val Asp Ser Ala
130 135 140

Ile Arg Asp Leu Ala Tyr His Asp Glu Ile Leu Ser Arg Met Lys Leu
145 150 155 160

Asn Glu Gln Leu Asn Lys Asp Ala Val Leu Ile Ile His Leu Gly Gly
165 170 175

Thr Phe Glu Gly Lys Lys Glu Thr Leu Asp Arg Phe Arg Lys Asn Tyr
180 185 190

Gln Arg Leu Ser Asp Ser Val Lys Ala Arg Leu Val Leu Glu Asn Asp
195 200 205

Asp Val Ser Trp Ser Val Gln Asp Leu Leu Pro Leu Cys Gln Glu Leu
210 215 220

Asn Ile Pro Leu Val Leu Asp Trp His His His Asn Ile Val Pro Gly
225 230 235 240

Thr Leu Arg Glu Gly Ser Leu Asp Leu Met Pro Leu Ile Pro Thr Ile
245 250 255

Arg Glu Thr Trp Thr Arg Lys Gly Ile Thr Gln Lys Gln His Tyr Ser
260 265 270

Glu Ser Ala Asp Pro Thr Ala Ile Ser Gly Met Lys Arg Arg Ala His
275 280 285

Ser Asp Arg Val Phe Asp Phe Pro Pro Cys Asp Pro Thr Met Asp Leu
290 295 300

Met Ile Glu Ala Lys Glu Lys Glu Gln Ala Val Phe Glu Leu Cys Arg
305 310 315 320

Arg Tyr Glu Leu Gln Asn Pro Pro Cys Pro Leu Glu Ile Met Gly Pro
325 330 335

Glu Tyr Asp Gln Thr Arg Asp Gly Tyr Tyr Pro Pro Gly Ala Glu Lys
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Arg Leu Thr Ala Arg Lys Arg Arg Ser Arg Lys Glu Glu Val Glu Glu
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Asp Glu Lys
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<210> 5
<211> 1811
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nucleotide
sequence encoding fusion protein of GST signal
peptide and the truncated version of S. pombe UVDE
protein.

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ggaacagggt gtatttgaat tgtgtagacg ttatgagtta caaatccac catgtcctct 1680
tgaaattatg gggcctgaat acgatcaaac tcgagatgga tattatccgc ccggagctga 1740
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<210> 6
 <211> 600
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein
 comprising the GST signal peptide and the
 truncated UVDE protein of *S. pombe*.

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 His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe
 35 40 45
 Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp
 50 55 60
 Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys
 65 70 75 80
 His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met
 85 90 95
 Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala
 100 105 110
 Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu
 115 120 125
 Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr
 130 135 140
 Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala
 145 150 155 160
 Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro
 165 170 175
 Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp
 180 185 190
 Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp
 195 200 205

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Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp His Leu
 210 215 220
 Val Pro Arg Gly Ser Asp Asp His Ala Pro Arg Glu Met Phe Asp Cys
 225 230 235 240
 Leu Asp Lys Pro Ile Pro Trp Arg Gly Arg Leu Gly Tyr Ala Cys Leu
 245 250 255
 Asn Thr Ile Leu Arg Ser Met Lys Glu Arg Val Phe Cys Ser Arg Thr
 260 265 270
 Cys Arg Ile Thr Thr Ile Gln Arg Asp Gly Leu Glu Ser Val Lys Gln
 275 280 285
 Leu Gly Thr Gln Asn Val Leu Asp Leu Ile Lys Leu Val Glu Trp Asn
 290 295 300
 His Asn Phe Gly Ile His Phe Met Arg Val Ser Ser Asp Leu Phe Pro
 305 310 315 320
 Phe Ala Ser His Ala Lys Tyr Gly Tyr Thr Leu Glu Phe Ala Gln Ser
 325 330 335
 His Leu Glu Glu Val Gly Lys Leu Ala Asn Lys Tyr Asn His Arg Leu
 340 345 350
 Thr Met His Pro Gly Gln Tyr Thr Gln Ile Ala Ser Pro Arg Glu Val
 355 360 365
 Val Val Asp Ser Ala Ile Arg Asp Leu Ala Tyr His Asp Glu Ile Leu
 370 375 380
 Ser Arg Met Lys Leu Asn Glu Gln Leu Asn Lys Asp Ala Val Leu Ile
 385 390 395 400
 Ile His Leu Gly Gly Thr Phe Glu Gly Lys Lys Glu Thr Leu Asp Arg
 405 410 415
 Phe Arg Lys Asn Tyr Gln Arg Leu Ser Asp Ser Val Lys Ala Arg Leu
 420 425 430
 Val Leu Glu Asn Asp Asp Val Ser Trp Ser Val Gln Asp Leu Leu Pro
 435 440 445
 Leu Cys Gln Glu Leu Asn Ile Pro Leu Val Leu Asp Trp His His His
 450 455 460
 Asn Ile Val Pro Gly Thr Leu Arg Glu Gly Ser Leu Asp Leu Met Pro
 465 470 475 480

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Leu Ile Pro Thr Ile Arg Glu Thr Trp Thr Arg Lys Gly Ile Thr Gln
485 490 495

Lys Gln His Tyr Ser Glu Ser Ala Asp Pro Thr Ala Ile Ser Gly Met
500 505 510

Lys Arg Arg Ala His Ser Asp Arg Val Phe Asp Phe Pro Pro Cys Asp
515 520 525

Pro Thr Met Asp Leu Met Ile Glu Ala Lys Glu Lys Glu Gln Ala Val
530 535 540

Phe Glu Leu Cys Arg Arg Tyr Glu Leu Gln Asn Pro Pro Cys Pro Leu
545 550 555 560

Glu Ile Met Gly Pro Glu Tyr Asp Gln Thr Arg Asp Gly Tyr Tyr Pro
565 570 575

Pro Gly Ala Glu Lys Arg Leu Thr Ala Arg Lys Arg Arg Ser Arg Lys
580 585 590

Glu Glu Val Glu Glu Asp Glu Lys
595 600

<210> 7

<211> 688

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence encoding GST signal peptide.

<400> 7

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tgataaatgg cgaaacaaaa agtttgaatt gggtttggag tttcccaatc ttccttatta 180
tattgatggg gatgttaaag taacacagtc tatggccatc atacgttata tagctgacaa 240
gcacaacatg ttggttgggt gtccaaaaga gcgtgcagag atttcaatgc ttgaaggagc 300
ggttttggat attagatacg gtgtttcgag aattgcataat agtaaagact ttgaaactct 360
caaagttgat tttcttagca agctacctga aatgctgaaa atgttcgaag atcgtttatg 420
tcataaaaaca tatttaaag ttgaccatgt aaccatcct gacttcatgt tgtatgacgc 480
tcttgatggt gttttataca tggacccaat gtgcctggat gcgttcccaa aattagtttg 540
ttttaaaaaa cgtattgaag ctatcccaca aattgataag tacttgaaat ccagcaagta 600
tatagcatgg cctttgcagg gctggcaagc cacgtttggg ggtggcgacc atcctccaaa 660
atcgatcat ctggttccgc gtggatcc 688
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<210> 8

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
sequence of GST signal peptide

<400> 8

Met Thr Lys Leu Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val
1 5 10 15

Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
20 25 30

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe
35 40 45

Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp
50 55 60

Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys
65 70 75 80

His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met
85 90 95

Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala
100 105 110

Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu
115 120 125

Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr
130 135 140

Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala
145 150 155 160

Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro
165 170 175

Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp
180 185 190

Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp
195 200 205

Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp His Leu
210 215 220

Val Pro Arg Gly Ser
225

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<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 9
tgaggatcca atcgttttca ttttttaatg cttagg 36

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 10
ggccatgggtt atttttcatc ctc 23

<210> 11
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 11
aatgggatcc gatgatcatg ctccacga 28

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 12
gggatcctta tttttcatcc ttttctac 28

<210> 13
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing cis-syn
cyclobutane pyrimidine dimer.

<220>
<221> misc_feature
<222> (15)..(16)
<223> At positions 15- 16, the T-T is in the form of
cis-syn cyclobutane pyrimidine dimer.

<400> 13
catgcctgca cgaattaagc aattcgtaat 30

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Undamaged
double stranded oligonucleotide.

<400> 14
catgcctgca cgaattaagc aattcgtaat 30

<210> 15
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing cis-syn
cyclobutane dimer at positions 21-22.

<400> 15
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcataagct 49

<210> 16
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing cis-syn
cyclobutane pyrimidine dimer at positions 21-22.

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"02250" 9624260

<400> 16
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 17
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing trans- syn 11
cyclobutane pyrimidine dimer at positions 21-22.

<400> 17
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 18
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing a 6-4 photo
product at position 21-22.

<400> 18
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 19
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing a Dewar
isomer.

<400> 19
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 20
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing cisplatin DNA
diadduct at position 16-17.

<400> 20
tccctccttc cttccggccc tccttccctt tc

32

<210> 21
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide wherein n is uracil at
position 21.

<220>
<221> misc_feature
<222> (21)
<223> The n at position 21 is uracil.

<400> 21
cttggactgg atgtcggcac nagcggatac aggagca

37

<210> 22
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide wherein n is
dihydrouracil at position 21.

<220>
<221> misc_feature
<222> (21)
<223> At position 21, n is dihydrouracil.

<400> 22
cttggactgg atgtcggcac nagcggatac aggagca

37

<210> 23
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide wherein n at position 21
represents an abasic site.

<220>
<221> misc_feature

<222> (21)
<223> At position 21, n is an abasic site.

<400> 23
cttgactgg atgtcggcac naggcgatac aggagca

37

<210> 24
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide wherein n at position 13
is an inosine.

<220>
<221> misc_feature
<222> (13)
<223> At position 13, n is inosine.

<400> 24
tgcaggctga ctnaggagga tccccgggta c

31

<210> 25
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide wherein n at position 13
is xanthine.

<220>
<221> misc_feature
<222> (13)
<223> N at position 13 is xanthine.

<400> 25
tgcaggctga ctnaggagga tccccgggta c

31

<210> 26
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide wherein n at position 21
is 8-oxoguanine.

<220>
 <221> misc_feature
 <222> (21)
 <223> N at position 21 is 8-oxoguanine.

 <400> 26
 cttggactgg atgtcggcac nagcggatac aggagca

37

<210> 27
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide representing all 16
 possible base pair mismatches at position 18 in
 individual preparations.

<220>
 <221> misc_feature
 <222> (18)
 <223> N at position 18 represents all 16 possible base
 pair mismatches.

<400> 27
 gtaccggggg atcctccnag tcgacctgca

30

<210> 28
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide containing a CA
 mismatched base pair at position 21.

<220>
 <221> misc_feature
 <222> (21)
 <223> N at position 21 represents C of C/A mismatched
 base pair.

<400> 28
 cgtagcatg cctgcacgaa ntaagcaatt cgtaatgcat t

41

<210> 29
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein there is a C/A mismatched base pair at position 36.

<220>

<221> misc_feature

<222> (36)

<223> N at position 36 represents a C/A mismatched base pair.

<400> 29

cgttacaagt ccgtcacgaa ttaagcaatt cgtaangcat t

41

<210> 30

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 31 represents a C/A mismatched base pair.

<220>

<221> misc_feature

<222> (31)

<223> The n at position 31 represents C of C/A mismatched base pair.

<400> 30

cgttacaagt ccgtcacgaa ttaagcaatt ngtaacgcat t

41

<210> 31

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 26 is a C/A mismatched base pair.

<220>

<221> misc_feature

<222> (26)

<223> N at position 26 represents a C/A mismatched base pair.

<400> 31

cgttacaagt ccgtcacgaa ttaagnaatt cgtaacgcat t

41

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<210> 32
<211> 41
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 21 is a C/A mismatched base pair.

<220>

<221> misc_feature

<222> (21)

<223> The n at position 21 represents a C/A mismatched base pair.

<400> 32

cgttacaagt ccgtcacgac ntaagcaatt cgtaacgcat t

41

<210> 33

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 15 represents a C/A mismatched base pair.

<220>

<221> misc_feature

<222> (15)

<223> The n at position 15 represents a C/A mismatched base pair.

<400> 33

cgttacaagt ccgtnacgaa ttaagcaatt cgtaacgcat t

41

<210> 34

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 10 is a C/A mismatched base pair.

<220>

<221> misc_feature

<222> (10)

<223> The n at position 10 represents a C/A mismatched base pair.

<400> 34

cggtacaagn ccgtcacgaa ttaagcaatt cgtaacgcat t

41

<210> 35

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 5 is a C/A mismatched base pair.

<220>

<221> misc_feature

<222> (5)

<223> The n at position 5 represents a C/A mismatched base pair.

<400> 35

cgtncaagt ccgtcacgaa ttaagcaatt cgtaacgcat t

41

<210> 36

<211> 656

<212> PRT

<213> Neurospora crassa

<400> 36

Met Pro Ser Arg Lys Ser Lys Ala Ala Ala Leu Asp Thr Pro Gln Ser
1 5 10 15

Glu Ser Ser Thr Phe Ser Ser Thr Leu Asp Ser Ser Ala Pro Ser Pro
20 25 30

Ala Arg Asn Leu Arg Arg Ser Gly Arg Asn Ile Leu Gln Pro Ser Ser
35 40 45

Glu Lys Asp Arg Asp His Glu Lys Arg Ser Gly Glu Glu Leu Ala Gly
50 55 60

Arg Met Met Gly Lys Asp Ala Asn Gly His Cys Leu Arg Glu Gly Lys
65 70 75 80

Glu Gln Glu Glu Gly Val Lys Met Ala Ile Glu Gly Leu Ala Arg Met
85 90 95

Glu Arg Arg Leu Gln Arg Ala Thr Lys Arg Gln Lys Lys Gln Leu Glu
100 105 110

Glu Asp Gly Ile Pro Val Pro Ser Val Val Ser Arg Phe Pro Thr Ala
 115 120 125
 Pro Tyr His His Lys Ser Thr Asn Ala Glu Glu Arg Glu Ala Lys Glu
 130 135 140
 Pro Val Leu Lys Thr His Ser Lys Asp Val Glu Arg Glu Ala Glu Ile
 145 150 155 160
 Gly Val Asp Asp Val Val Lys Met Glu Pro Ala Ala Thr Asn Ile Ile
 165 170 175
 Glu Pro Glu Asp Ala Gln Asp Ala Ala Glu Arg Gly Ala Ala Arg Pro
 180 185 190
 Pro Ala Val Asn Ser Ser Tyr Leu Pro Leu Pro Trp Lys Gly Arg Leu
 195 200 205
 Gly Tyr Ala Cys Leu Asn Thr Tyr Leu Arg Asn Ala Lys Pro Pro Ile
 210 215 220
 Phe Ser Ser Arg Thr Cys Arg Met Ala Ser Ile Val Asp His Arg His
 225 230 235 240
 Pro Leu Gln Phe Glu Asp Glu Pro Glu His His Leu Lys Asn Lys Pro
 245 250 255
 Asp Lys Ser Lys Glu Pro Gln Asp Glu Leu Gly His Lys Phe Val Gln
 260 265 270
 Glu Leu Gly Leu Ala Asn Ala Arg Asp Ile Val Lys Met Leu Cys Trp
 275 280 285
 Asn Glu Lys Tyr Gly Ile Arg Phe Leu Arg Leu Ser Ser Glu Met Phe
 290 295 300
 Pro Phe Ala Ser His Pro Val His Gly Tyr Lys Leu Ala Pro Phe Ala
 305 310 315 320
 Ser Glu Val Leu Ala Glu Ala Gly Arg Val Ala Ala Glu Leu Gly His
 325 330 335
 Arg Leu Thr Thr His Pro Gly Gln Phe Thr Gln Leu Gly Ser Pro Arg
 340 345 350
 Lys Glu Val Val Glu Ser Ala Ile Arg Asp Leu Glu Tyr His Asp Glu
 355 360 365
 Leu Leu Ser Leu Leu Lys Leu Pro Glu Gln Gln Asn Arg Asp Ala Val
 370 375 380

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102250" 95242260

Met	Ile	Ile	His	Met	Gly	Gly	Gln	Phe	Gly	Asp	Lys	Ala	Ala	Thr	Leu	385	390	395	400
Glu	Arg	Phe	Lys	Arg	Asn	Tyr	Ala	Arg	Leu	Ser	Gln	Ser	Cys	Lys	Asn	405	410	415	
Arg	Leu	Val	Leu	Glu	Asn	Asp	Asp	Val	Gly	Trp	Thr	Val	His	Asp	Leu	420	425	430	
Leu	Pro	Val	Cys	Glu	Glu	Leu	Asn	Ile	Pro	Met	Val	Leu	Asp	Tyr	His	435	440	445	
His	His	Asn	Ile	Cys	Phe	Asp	Pro	Ala	His	Leu	Arg	Glu	Gly	Thr	Leu	450	455	460	
Asp	Ile	Ser	Asp	Pro	Lys	Leu	Gln	Glu	Arg	Ile	Ala	Asn	Thr	Trp	Lys	465	470	475	480
Arg	Lys	Gly	Ile	Lys	Gln	Lys	Met	His	Tyr	Ser	Glu	Pro	Cys	Asp	Gly	485	490	495	
Ala	Val	Thr	Pro	Arg	Asp	Arg	Arg	Lys	His	Arg	Pro	Arg	Val	Met	Thr	500	505	510	
Leu	Pro	Pro	Cys	Pro	Pro	Asp	Met	Asp	Leu	Met	Ile	Glu	Ala	Lys	Asp	515	520	525	
Lys	Glu	Gln	Ala	Val	Phe	Glu	Leu	Met	Arg	Thr	Phe	Lys	Leu	Pro	Gly	530	535	540	
Phe	Glu	Lys	Ile	Asn	Asp	Met	Val	Pro	Tyr	Asp	Arg	Asp	Asp	Glu	Asn	545	550	555	560
Arg	Pro	Ala	Pro	Pro	Val	Lys	Ala	Pro	Lys	Lys	Lys	Lys	Gly	Gly	Lys	565	570	575	
Arg	Lys	Arg	Thr	Thr	Asp	Glu	Glu	Ala	Ala	Glu	Pro	Glu	Glu	Val	Asp	580	585	590	
Thr	Ala	Ala	Asp	Asp	Val	Lys	Asp	Ala	Pro	Glu	Gly	Pro	Lys	Glu	Val	595	600	605	
Pro	Glu	Glu	Glu	Arg	Ala	Met	Gly	Gly	Pro	Tyr	Asn	Arg	Val	Tyr	Trp	610	615	620	
Pro	Leu	Gly	Cys	Glu	Glu	Trp	Leu	Lys	Pro	Lys	Lys	Arg	Glu	Val	Lys	625	630	635	640
Lys	Gly	Lys	Val	Pro	Glu	Glu	Val	Glu	Asp	Glu	Gly	Glu	Phe	Asp	Gly	645	650	655	

<210> 37
 <211> 317
 <212> PRT
 <213> Bacillus subtilis

<400> 37
 Met Ile Phe Arg Phe Gly Phe Val Ser Asn Ala Met Ser Leu Trp Asp
 1 5 10 15
 Ala Ser Pro Ala Lys Thr Leu Thr Phe Ala Arg Tyr Ser Lys Leu Ser
 20 25 30
 Lys Thr Glu Arg Lys Glu Ala Leu Leu Thr Val Thr Lys Ala Asn Leu
 35 40 45
 Arg Asn Thr Met Arg Thr Leu His Tyr Ile Ile Gly His Gly Ile Pro
 50 55 60
 Leu Tyr Arg Phe Ser Ser Ser Ile Val Pro Leu Ala Thr His Pro Asp
 65 70 75 80
 Val Met Trp Asp Phe Val Thr Pro Phe Gln Lys Glu Phe Arg Glu Ile
 85 90 95
 Gly Glu Leu Val Lys Thr His Gln Leu Arg Thr Ser Phe His Pro Asn
 100 105 110
 Gln Phe Thr Leu Phe Thr Ser Pro Lys Glu Ser Val Thr Lys Asn Ala
 115 120 125
 Val Thr Asp Met Ala Tyr His Tyr Arg Met Leu Glu Ala Met Gly Ile
 130 135 140
 Ala Asp Arg Ser Val Ile Asn Ile His Ile Gly Gly Ala Tyr Gly Asn
 145 150 155 160
 Lys Asp Thr Ala Thr Ala Gln Phe His Gln Asn Ile Lys Gln Leu Pro
 165 170 175
 Gln Glu Ile Lys Glu Arg Met Thr Leu Glu Asn Asp Asp Lys Thr Tyr
 180 185 190
 Thr Thr Glu Glu Thr Leu Gln Val Cys Glu Gln Glu Asp Val Pro Phe
 195 200 205
 Val Phe Asp Phe His His Phe Tyr Ala Asn Pro Asp Asp His Ala Asp
 210 215 220

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Leu Asn Val Ala Leu Pro Arg Met Ile Lys Thr Trp Glu Arg Ile Gly
225 230 235 240

Leu Gln Pro Lys Val His Leu Ser Ser Pro Lys Ser Glu Gln Ala Ile
245 250 255

Arg Ser His Ala Asp Tyr Val Asp Ala Asn Phe Leu Leu Glu Arg Phe
260 265 270

Arg Gln Trp Gly Thr Asn Ile Asp Phe Met Ile Glu Ala Lys Gln Lys
275 280 285

Asp Lys Ala Leu Leu Arg Leu Met Asp Glu Leu Ser Ser Ile Arg Gly
290 295 300

Val Lys Arg Ile Gly Gly Gly Ala Leu Gln Trp Lys Ser
305 310 315

<210> 38

<211> 580

<212> PRT

<213> Homo sapiens

<400> 38

Met Gly Thr Thr Gly Leu Glu Ser Leu Ser Leu Gly Asp Arg Gly Ala
1 5 10 15

Ala Pro Thr Val Thr Ser Ser Glu Arg Leu Val Pro Asp Pro Pro Asn
20 25 30

Asp Leu Arg Lys Glu Asp Val Ala Met Glu Leu Glu Arg Val Gly Glu
35 40 45

Asp Glu Glu Gln Met Met Ile Lys Arg Ser Ser Glu Cys Asn Pro Leu
50 55 60

Leu Gln Glu Pro Ile Ala Ser Ala Gln Phe Gly Ala Thr Ala Gly Thr
65 70 75 80

Glu Cys Arg Lys Ser Val Pro Cys Gly Trp Glu Arg Val Val Lys Gln
85 90 95

Arg Leu Phe Gly Lys Thr Ala Gly Arg Phe Asp Val Tyr Phe Ile Ser
100 105 110

Pro Gln Gly Leu Lys Phe Arg Ser Lys Ser Ser Leu Ala Asn Tyr Leu
115 120 125

His Lys Asn Gly Glu Thr Ser Leu Lys Pro Glu Asp Phe Asp Phe Thr
130 135 140

09724256 "052701

Val	Leu	Ser	Lys	Arg	Gly	Ile	Lys	Ser	Arg	Tyr	Lys	Asp	Cys	Ser	Met	145	150	155	160
Ala	Ala	Leu	Thr	Ser	His	Leu	Gln	Asn	Gln	Ser	Asn	Asn	Ser	Asn	Trp	165	170	175	
Asn	Leu	Arg	Thr	Arg	Ser	Lys	Cys	Lys	Lys	Asp	Val	Phe	Met	Pro	Pro	180	185	190	
Ser	Ser	Ser	Ser	Glu	Leu	Gln	Glu	Ser	Arg	Gly	Leu	Ser	Asn	Phe	Thr	195	200	205	
Ser	Thr	His	Leu	Leu	Leu	Lys	Glu	Asp	Glu	Gly	Val	Asp	Asp	Val	Asn	210	215	220	
Phe	Arg	Lys	Val	Arg	Lys	Pro	Lys	Gly	Lys	Val	Thr	Ile	Leu	Lys	Gly	225	230	235	240
Ile	Pro	Ile	Lys	Lys	Thr	Lys	Lys	Gly	Cys	Arg	Lys	Ser	Cys	Ser	Gly	245	250	255	
Phe	Val	Gln	Ser	Asp	Ser	Lys	Arg	Glu	Ser	Val	Cys	Asn	Lys	Ala	Asp	260	265	270	
Ala	Glu	Ser	Glu	Pro	Val	Ala	Gln	Lys	Ser	Gln	Leu	Asp	Arg	Thr	Val	275	280	285	
Cys	Ile	Ser	Asp	Ala	Gly	Ala	Cys	Gly	Glu	Thr	Leu	Ser	Val	Thr	Ser	290	295	300	
Glu	Glu	Asn	Ser	Leu	Val	Lys	Lys	Lys	Glu	Arg	Ser	Leu	Ser	Ser	Gly	305	310	315	320
Ser	Asn	Phe	Cys	Ser	Glu	Gln	Lys	Thr	Ser	Gly	Ile	Ile	Asn	Lys	Phe	325	330	335	
Cys	Ser	Ala	Lys	Asp	Ser	Glu	His	Asn	Glu	Lys	Tyr	Glu	Asp	Thr	Phe	340	345	350	
Leu	Glu	Ser	Glu	Glu	Ile	Gly	Thr	Lys	Val	Glu	Val	Val	Glu	Arg	Lys	355	360	365	
Glu	His	Leu	His	Thr	Asp	Ile	Leu	Lys	Arg	Gly	Ser	Glu	Met	Asp	Asn	370	375	380	
Asn	Cys	Ser	Pro	Thr	Arg	Lys	Asp	Phe	Thr	Gly	Glu	Lys	Ile	Phe	Gln	385	390	395	400
Glu	Asp	Thr	Ile	Pro	Arg	Thr	Gln	Ile	Glu	Arg	Arg	Lys	Thr	Ser	Leu	405	410	415	

Tyr Phe Ser Ser Lys Tyr Asn Lys Glu Ala Leu Ser Pro Pro Arg Arg
420 425 430

Lys Ala Phe Lys Lys Trp Thr Pro Pro Arg Ser Pro Phe Asn Leu Val
435 440 445

Gln Glu Thr Leu Phe His Asp Pro Trp Lys Leu Leu Ile Ala Thr Ile
450 455 460

Phe Leu Asn Arg Thr Ser Gly Lys Met Ala Ile Pro Val Leu Trp Lys
465 470 475 480

Phe Leu Glu Lys Tyr Pro Ser Ala Glu Val Ala Arg Thr Ala Asp Trp
485 490 495

Arg Asp Val Ser Glu Leu Leu Lys Pro Leu Gly Leu Tyr Asp Leu Arg
500 505 510

Ala Lys Thr Ile Val Lys Phe Ser Asp Glu Tyr Leu Thr Lys Gln Trp
515 520 525

Lys Tyr Pro Ile Glu Leu His Gly Ile Gly Lys Tyr Gly Asn Asp Ser
530 535 540

Tyr Arg Ile Phe Cys Val Asn Glu Trp Lys Gln Val His Pro Glu Asp
545 550 555 560

His Lys Leu Asn Lys Tyr His Asp Trp Leu Trp Glu Asn His Glu Lys
565 570 575

Leu Ser Leu Ser
580

<210> 39

<211> 294

<212> PRT

<213> Deinococcus radiodurans

<400> 39

Gln Leu Gly Leu Val Cys Leu Thr Val Gly Pro Glu Val Arg Phe Arg
1 5 10 15

Thr Val Thr Leu Ser Arg Tyr Arg Ala Leu Ser Pro Ala Glu Arg Glu
20 25 30

Ala Lys Leu Leu Asp Leu Tyr Ser Ser Asn Ile Lys Thr Leu Arg Gly
35 40 45

Ala Ala Asp Tyr Cys Ala Ala His Asp Ile Arg Leu Tyr Arg Leu Ser
50 55 60

Ser Ser Leu Phe Pro Met Leu Asp Leu Ala Gly Asp Asp Thr Gly Ala
 65 70 75 80
 Ala Val Leu Thr His Leu Ala Pro Gln Leu Leu Glu Ala Gly His Ala
 85 90 95
 Phe Thr Asp Ala Gly Val Arg Leu Leu Met His Pro Glu Gln Phe Ile
 100 105 110
 Val Leu Asn Ser Asp Arg Pro Glu Val Arg Glu Ser Ser Val Arg Ala
 115 120 125
 Met Ser Ala His Ala Arg Val Met Asp Gly Leu Gly Leu Ala Arg Thr
 130 135 140
 Pro Trp Asn Leu Leu Leu Leu His Gly Gly Lys Gly Gly Arg Gly Ala
 145 150 155 160
 Glu Leu Ala Ala Leu Ile Pro Asp Leu Pro Asp Pro Val Arg Leu Arg
 165 170 175
 Leu Gly Leu Glu Asn Asp Glu Arg Ala Tyr Ser Pro Ala Glu Leu Leu
 180 185 190
 Pro Ile Cys Glu Ala Thr Gly Thr Pro Leu Val Phe Asp Ala His His
 195 200 205
 His Val Val His Asp Lys Leu Pro Asp Gln Glu Asp Pro Ser Val Arg
 210 215 220
 Glu Trp Val Leu Arg Ala Arg Ala Thr Trp Gln Pro Pro Glu Trp Gln
 225 230 235 240
 Val Val His Leu Ser Asn Gly Ile Glu Gly Pro Gln Asp Arg Arg His
 245 250 255
 Ser His Leu Ile Ala Asp Phe Pro Ser Ala Tyr Ala Asp Val Pro Gln
 260 265 270
 Ile Glu Val Glu Ala Lys Gly Lys Glu Glu Ala Ile Ala Ala Leu Arg
 275 280 285
 Leu Met Ala Pro Phe Lys
 290

<210> 40

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 40

cacagactcc ctctgtcata ggtttgagtt tatatggaa

39

<210> 41

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 41

ttccatataa actcaaacct atgacagagg gagtctgtg

39

<210> 42

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 42

cacagactcc ctctgtcata ggttcatgag tttatatgga a

41

<210> 43

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 43

cacagactcc ctctgtcata ggttcacatg agtttatatg gaa

43

<210> 44

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

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102250" 96242260

<400> 44
cacagactcc ctctgtcata gggtcacaca tgagtttata tggaa 45

<210> 45
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 45
cacagactcc ctctgtcata gggtcacaca catgagttta tatggaa 47

<210> 46
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 46
cacagactcc ctctgtcata gggtgagtac tagtactctg agtttatatg gaa 53

<210> 47
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 47
cgttagaact ccgtcacgaa ttaagcaatt agtaatgcat t 41

<210> 48
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 48
aatgcattac taattgctta attcgtgacg gagttctaac g 41

<210> 49
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 49 43
cgttagaact ccgtcacgaa ttaagcaatt caagtaatgc att

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 50 45
cgttagaact ccgtcacgaa ttaagcaatt cacaagtaat gcatt

<210> 51
<211> 47
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Oligonucleotide

<400> 51 47
cgttagaact ccgtcacgaa ttaagcaatt cacacaagta atgcatt

<210> 52
<211> 49
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Oligonucleotide

<400> 52 49
cgttagaact ccgtcacgaa ttaagcaatt cacacacaag taatgcatt

<210> 53
<211> 41
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 53

cgttacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t

41

<210> 54

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
Oligonucleotide

<400> 54

aatgcattac gaattgctta attcgtgacg gacttgtaac g

41

<210> 55

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
Oligonucleotide

<400> 55

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41

<210> 56

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
Oligonucleotide

<400> 56

aatgcgttac aaattgctta attcgtgacg gacttgtaac g

41

<210> 57

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

09734296-052701

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 57
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<210> 58
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 58
aatgcgttac gaattactta attcgtgacg gacttgtaac g 41

<210> 59
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<212> DNA
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<220>
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Oligonucleotide

<400> 59
cgttacaagt ccgtcacgac ttaagcaatt cgtaacgcat t 41

<210> 60
<211> 41
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<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 60
aatgcgttac gaattgctta aatcgtgacg gacttgtaac g 41

<210> 61
<211> 41
<212> DNA
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<220>
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Oligonucleotide

00724296 052704
T02250 9624260

<400> 61
cgttacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 62
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 62
aatgcggttac gaattgctta attcgtaacg gacttgtaac g 41

<210> 63
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 63
cgttacaagc ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 64
<211> 41
<212> DNA
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<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 64
aatgcggttac gaattgctta attcgtgacg gacttgtaac g 41

<210> 65
<211> 41
<212> DNA
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<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 65
cgttccaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 66
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 66
aatgcgttac gaattgctta attcgtgacg gacttgaaac g 41

<210> 67
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 67
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tgcactcgac gatagtct 78

<210> 68
<211> 49
<212> DNA
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<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 68
tgcagtgtgc gaattctgtc ccatcatcac atccggatcg ttcggttct 49

<210> 69
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 69
gactatcgtg cagtgcagtg tgcgaattct gtcccatcat cacatccgga tcgttcggtt 60
ct 62

<210> 70

<211> 64
<212> DNA
<213> Artificial Sequence

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Oligonucleotide

<400> 70
tgcagtgtgc gaattctgtc ccatcatcac atccggatcg ttcggttctc tcgaggtccg 60
tgca 64

<210> 71
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
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Oligonucleotide

<400> 71
gagactatcg tgcagtgcag tgtgcgaatt ctgtcccatc atcacatccg gatcgttcgg 60
ttctctcgag gtccgtgca 79

0974296-052701
T02250" 9624260